

PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,008

DATE: 06/18/2001

TIME: 16:10:31

Input Set : A:\ES.txt

Output Set : N:\CRF3\06182001\I857008.raw

Does Not Comply
Correct: Discrete Nucleic

3 <110> APPLICANT: Herscovici, Jean
 4 Hofland, Hans
 5 Jacopin, Christophe
 6 Scherman, Daniel
 8 <120> TITLE OF INVENTION: NOVEL NUCLEIC ACID TRANSFERRING AGENTS, COMPOSITIONS
 CONTAINING THEM AND
 9 USES

11 <130> FILE REFERENCE: ST98046PCT-US
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/857,008

14 <141> CURRENT FILING DATE: 2001-05-30
 16 <150> PRIOR APPLICATION NUMBER: PCI/FR99/02995
 17 <151> PRIOR FILING DATE: 1999-12-02
 19 <150> PRIOR APPLICATION NUMBER: US 60/117,184
 20 <151> PRIOR FILING DATE: 1999-01-26
 22 <150> PRIOR APPLICATION NUMBER: FR 98/15,309
 23 <151> PRIOR FILING DATE: 1998-12-03
 25 <160> NUMBER OF SEQ ID NOS: 2

27 <170> SOFTWARE: PatentIn version 3.0
 29 <210> SEQ ID NO: 1

30 <211> LENGTH: 9

31 <212> TYPE: PRT

32 <213> ORGANISM: none

34 <400> SEQUENCE: 1

36 Lys Thr Pro Lys Lys Ala Lys Lys Pro

37 1 5

39 <210> SEQ ID NO: 2

40 <211> LENGTH: 8

41 <212> TYPE: PRT

42 <213> ORGANISM: none

44 <400> SEQUENCE: 2

46 Ala Thr Pro Ala Lys Lys Ala Ala

47 2 5

Per 1.823 of Sequence Rules, see item 10 on

*Even
summary
sheet*

incubated

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/857,008

DATE: 06/18/2001

TIME: 16:10:32

Input Set : A:\ES.txt

Output Set : N:\CRF3\06182001\I857008.raw

1:13 M:270 C: Current Application Number differs. Replaced Current Application Number

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/857003

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species) <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32). (See 1.823 of Sequence Rules)